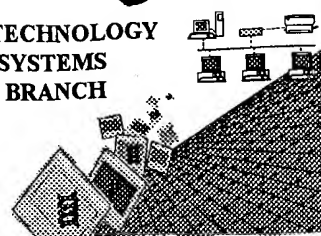


650-622-2499

BIOTECHNOLOGY
SYSTEMS
BRANCH



#15
pg 5/8/02

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/59,466B 11634
Source: 1620
Date Processed by STIC: 4/29/2002

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/59,466B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

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FYI



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,466B

DATE: 04/29/2002
TIME: 16:40:33

pg 1-3

Input Set : A:\032266-003.ST25.txt
Output Set: N:\CRF3\04292002\I591466B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Von Schaewen, Antje
5 <120> TITLE OF INVENTION: Plant GntI Sequences and the Use Thereof for the Production
6 of Plants Having Reduced or Lacking N-acetyl Glucosaminyl
7 Transferase I(GntI) Activity
9 <130> FILE REFERENCE: 032266-003
11 <140> CURRENT APPLICATION NUMBER: US 09/591,466B
12 <141> CURRENT FILING DATE: 2000-06-09
14 <150> PRIOR APPLICATION NUMBER: EP 98/08001
15 <151> PRIOR FILING DATE: 1998-09-12
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

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ERRORED SEQUENCES

447 <210> SEQ ID NO: 4
448 <211> LENGTH: 446
449 <212> TYPE: PRT
450 <213> ORGANISM: Nicotiana tabacum
E--> 452 <400> SEQUENCE: *46 insert 4*
453 Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu Ile Leu
454 1 5 10 15
455 Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala Thr Gln
456 20 25 30
457 Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His
458 35 40 45
459 Cys Thr Ser Gln Thr Arg Leu Ile Asp Gln Ile Ser Leu Gln Gln
460 50 55 60
461 Gly Arg Ile Val Ala Leu Glu Glu Met Lys Arg Gln Asp Gln Glu
462 65 70 75 80
463 Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
464 85 90 95
465 Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val Val
466 100 105 110
467 Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile
468 115 120 125
469 Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
470 130 135 140
471 Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp
472 145 150 155 160
473 Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu
474 165 170 175
475 Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys

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*(only the errored portion of
Sequence 4
is shown)*

<210> 1
 <211> 1669
 <212> DNA
 <213> Solanum tuberosum

<220>
 <221> misc_feature
 <222> (659)...(667)
 <223> function: Asn codon in this context is a potential
 glycosylation site;
 product: N-glycosylation consensus sequence;
 phenotype: N-glycans modulate protein properties;
 standard_name: N-glycosylation site;
 label: pot-CHO;
 note: GnTI-coding sequences from animals do not
 contain this feature.

global err

insert
 <220> ←

misspelled - replace
 with "glycosylation"

Per 1.823 of Sequence Rules, each
 <223> section has a maximum of 4 lines.

Please insert a <220> after each group of
4 lines.

IMPORTANT
 →

The types of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

09/09/1,466B 3

<210> 6
<211> 444
<212> PRT
<213> ←
<400> 6

insert this mandatory numeric identifier and its response

(see item 10 on Error Summary Sheet)

PJ I

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.